

OIPE
ENTEREDRAW SEQUENCE LISTING
PATENT APPLICATION: US/10/085,188DATE: 03/19/2002
TIME: 15:53:43Input Set : A:\98-69C1.SEQ.txt
Output Set: N:\CRF3\03192002\J085188.raw

4 <110> APPLICANT: Presnell, Scott R.
 5 Taft, David W.
 7 <120> TITLE OF INVENTION: A New Member of the Human
 8 Syntaxin/Epinorphin Family
 10 <130> FILE REFERENCE: 98-69
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/085,188
 C--> 12 <141> CURRENT FILING DATE: 2002-02-26
 12 <160> NUMBER OF SEQ ID NOS: 9
 14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1274
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (189)...(1049)
 25 <400> SEQUENCE: 1
 26 gcggccgcgg cggcgcggag ctcgggcggc cgtggaggaa ctcagcctcg gccgcaggag 60
 27 gcgccgggag cggagccgccc gggagtcgcg caacaggtt cttctccat cgctgcgccc 120
 28 acaggggacg cgcgcctgc cgggagaggg gcttctcggt tcgcactctc gotcccagtc 180
 29 caggcaaa atg aaa gac cgg cta gca gaa ctt ctg gac ttg tcc aag caa 230
 30 Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln
 31 1 5 10
 33 tat gac cag cag ttc cca gac ggg gac gat gag ttt gac tcg ccc cac 278
 34 Tyr Asp Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His
 35 15 20 25 30
 37 gag gac atc gtg ttc gag acg gac cac atc ctg gag tcc ctg tac cga 326
 38 Glu Asp Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg
 39 35 40 45
 41 gac atc cgg gac att cag gat gaa aac cag ctg ctg gtg gcc gac gtg 374
 42 Asp Ile Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val
 43 50 55 60
 45 aag cgg ctg gga aag cag aac gcc cgc ttc ctc acg tcc atg cgg cgc 422
 46 Lys Arg Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg
 47 65 70 75
 49 ctc agc agc atc aag cgc gac acc aac tcc atc gcc aag gcc atc aag 470
 50 Leu Ser Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys
 51 80 85 90
 53 gcc cgg ggc gag gtc atc cac tgc aag ctg cgc gcc atg aag gag ctg 518
 54 Ala Arg Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu
 55 95 100 105 110
 57 agc gag gcg gct gag gcc cag cac ggc ccg cac tcg gca gtg gcg cgc 566
 58 Ser Glu Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg

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| | | | | |
|-----|--|-----|-----|------|
| 59 | 115 | 120 | 125 | |
| 61 | att tcg cgg gcg cag tac aac gcg ctc acc ctc acc ttc cag cgc gcc | | | 614 |
| 62 | Ile Ser Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala | | | |
| 63 | 130 | 135 | 140 | |
| 65 | atg cac gac tac aac cag gcc gag atg aag cag cgc gac aac tgc aag | | | 662 |
| 66 | Met His Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys | | | |
| 67 | 145 | 150 | 155 | |
| 69 | atc cgc atc cag cgc cag ctg gag atc atg ggc aag gaa gtc tcg ggc | | | 710 |
| 70 | Ile Arg Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly | | | |
| 71 | 160 | 165 | 170 | |
| 73 | gac cag atc gag gac atg ttc gag cag ggt aag tgg gac gtg ttt tcc | | | 758 |
| 74 | Asp Gln Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser | | | |
| 75 | 175 | 180 | 185 | 190 |
| 77 | gag aac ttg ctg gcc gac gtg aag ggc gcg cggt gcc ctc aac gag | | | 806 |
| 78 | Glu Asn Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu | | | |
| 79 | 195 | 200 | 205 | |
| 81 | atc gag agc cgc cac cgc gaa ctg ctg cgc ctg gag agc cgc atc cgc | | | 854 |
| 82 | Ile Glu Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg | | | |
| 83 | 210 | 215 | 220 | |
| 85 | gac gta cac gag ctc ttc ttg cag atg gcg gtg ctg gtg gag aag cag | | | 902 |
| 86 | Asp Val His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln | | | |
| 87 | 225 | 230 | 235 | |
| 89 | gcc gac acc ctg aac gtc atc gag ctc aac gta caa aag acg gtc gac | | | 950 |
| 91 | Ala Asp Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp | | | |
| 92 | 240 | 245 | 250 | |
| 94 | tac acc ggc cag gcc aag gcg cag gtg cgg aag gcc gtg cag tac gag | | | 998 |
| 95 | Tyr Thr Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu | | | |
| 96 | 255 | 260 | 265 | 270 |
| 98 | gag aag aac ccc tgc cgg acc ctc tgc tgc ttc tgc tgt ccc tgc ctc | | | 1046 |
| 99 | Glu Lys Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu | | | |
| 100 | 275 | 280 | 285 | |
| 102 | aag tagcaggccg gcccccggccg ccaccggcca tccccagacca tggagcgccgc | | | 1099 |
| 103 | tgggaaggac gcaccaaagc cgggagctct gcccctgcagg gagttggccc aaccctttcc | | | 1159 |
| 104 | ggaactcagt cttagaaaaa gaaacgcccag gttcaagaat tgcaaaccag cctgtgcttg | | | 1219 |
| 105 | gaaagatggt tagttgatac cgtccgatga ttcttcagta aagatagatt cccac | | | 1274 |
| 107 | <210> SEQ ID NO: 2 | | | |
| 108 | <211> LENGTH: 287 | | | |
| 109 | <212> TYPE: PRT | | | |
| 110 | <213> ORGANISM: Homo sapiens | | | |
| 112 | <400> SEQUENCE: 2 | | | |
| 113 | Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp | | | |
| 114 | 1 | 5 | 10 | 15 |
| 115 | Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp | | | |
| 116 | 20 | 25 | 30 | |
| 117 | Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile | | | |
| 118 | 35 | 40 | 45 | |
| 119 | Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg | | | |
| 120 | 50 | 55 | 60 | |
| 121 | Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser | | | |

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| | | | | |
|-----|---|-----|-----|-----|
| 122 | 65 | 70 | 75 | 80 |
| 123 | Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg | | | |
| 124 | 85 | 90 | 95 | |
| 125 | Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu | | | |
| 126 | 100 | 105 | 110 | |
| 127 | Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser | | | |
| 128 | 115 | 120 | 125 | |
| 129 | Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His | | | |
| 130 | 130 | 135 | 140 | |
| 131 | Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg | | | |
| 132 | 145 | 150 | 155 | 160 |
| 133 | Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln | | | |
| 134 | 165 | 170 | 175 | |
| 136 | Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn | | | |
| 137 | 180 | 185 | 190 | |
| 138 | Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu | | | |
| 139 | 195 | 200 | 205 | |
| 140 | Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val | | | |
| 141 | 210 | 215 | 220 | |
| 142 | His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp | | | |
| 143 | 225 | 230 | 235 | 240 |
| 144 | Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr | | | |
| 145 | 245 | 250 | 255 | |
| 146 | Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys | | | |
| 147 | 260 | 265 | 270 | |
| 148 | Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu Lys | | | |
| 149 | 275 | 280 | 285 | |

151 <210> SEQ ID NO: 3

152 <211> LENGTH: 861

153 <212> TYPE: DNA

154 <213> ORGANISM: Artificial Sequence

156 <220> FEATURE:

157 <223> OTHER INFORMATION: This degenerate sequence encodes the amino acid sequence of SEQ ID NO:2.

160 <221> NAME/KEY: variation

161 <222> LOCATION: (1)...(861)

162 <223> OTHER INFORMATION: N is any nucleotide.

164 <400> SEQUENCE: 3

| | | |
|----------|---|-----|
| W--> 165 | atgaargaym gnytngcnga rytnytnay ytnwsnaarc artaygayca rcarttyccn | 60 |
| W--> 166 | gayggngayg aygarttyga ywsncncay gargayathg tnttygarac ngaycayath | 120 |
| W--> 167 | ytnigarwsny tntaymgngay yathmgngay athcargayg araaycaryt nytngtngcn | 180 |
| W--> 168 | gaygttnaarm gnytnngnaa rcaraaygcn mgntyyttna cnwsnatgmg nmgnytwnsn | 240 |
| W--> 169 | wsnathaarm gngayacnaa ywsnathgcn aargcnatha argcnmgngg ngargtnath | 300 |
| W--> 170 | caytgyaary tnmngncnat gaargarytn wsngargcng cngargcnca rcayggncn | 360 |
| W--> 171 | caywsngcng tngcnmgnat hwsnmngcn cartayaayg cnytnacnyt nacnttycar | 420 |
| W--> 172 | mgngcnatgc ayygatayaa ycargcngar atgaarcarm gngayaaytg yaarathmgn | 480 |
| W--> 173 | athcarmgnc arytngarat hatgggnaar gargtnwsng gngaycarat hgargayatg | 540 |
| W--> 174 | ttygarcarg gnaartggga ygtnttywsn garaayytny tngcngaygt naarggngcn | 600 |
| W--> 175 | mgngcngcny tnaaygarat hgarwsnmgn caymgngary tnytnmgnyt ngarwshmgn | 660 |

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| | | | |
|----------|---|------------------------------------|-----|
| W--> 176 | athmgngayg tncaygaryt nttyytnca | atggcngtny tngtngaraa rcargcngay | 720 |
| W--> 177 | acnytnaayg tnathgaryt naaygtncar | aaracngtng aytayacngg ncargcnaar | 780 |
| W--> 178 | gcncargtnm gnaargcngt ncartaygar | garaaraaayc cntgymgnac nyntntgytgy | 840 |
| W--> 179 | ttytgytgyc cntgyytnaa r | | 861 |
| 181 | <210> SEQ ID NO: 4 | | |
| 182 | <211> LENGTH: 18 | | |
| 183 | <212> TYPE: DNA | | |
| 184 | <213> ORGANISM: Artificial Sequence | | |
| 186 | <220> FEATURE: | | |
| 187 | <223> OTHER INFORMATION: PCR primer | | |
| 189 | <400> SEQUENCE: 4 | | |
| 190 | tggcggtgct ggtggaga | | 18 |
| 192 | <210> SEQ ID NO: 5 | | |
| 193 | <211> LENGTH: 18 | | |
| 194 | <212> TYPE: DNA | | |
| 195 | <213> ORGANISM: Artificial Sequence | | |
| 197 | <220> FEATURE: | | |
| 198 | <223> OTHER INFORMATION: PCR primer | | |
| 200 | <400> SEQUENCE: 5 | | |
| 201 | ccggcagggg ttcttc | | 18 |
| 203 | <210> SEQ ID NO: 6 | | |
| 204 | <211> LENGTH: 287 | | |
| 205 | <212> TYPE: PRT | | |
| 206 | <213> ORGANISM: Homo sapiens | | |
| 208 | <400> SEQUENCE: 6 | | |
| 209 | Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp | | |
| 210 | 1 5 10 15 | | |
| 211 | Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp | | |
| 212 | 20 25 30 | | |
| 213 | Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile | | |
| 214 | 35 40 45 | | |
| 215 | Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asn Val Lys Arg | | |
| 216 | 50 55 60 | | |
| 217 | Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser | | |
| 218 | 65 70 75 80 | | |
| 219 | Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Pro | | |
| 220 | 85 90 95 | | |
| 221 | Pro Glu Val Ile His Cys Asn Val Arg Ala Met Lys Glu Leu Ser Glu | | |
| 222 | 100 105 110 | | |
| 223 | Ala Ala Glu Ala Gln His Gly Pro Ala Leu Gly Ser Gly Gly Ile Ser | | |
| 224 | 115 120 125 | | |
| 226 | Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His | | |
| 227 | 130 135 140 | | |
| 228 | Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg | | |
| 229 | 145 150 155 160 | | |
| 230 | Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln | | |
| 231 | 165 170 175 | | |
| 232 | Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn | | |
| 233 | 180 185 190 | | |

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234 Leu Leu Ala Asp Val Lys Gly Val Arg Ala Ala Leu Asn Glu Ile Glu
235 195 200 205
236 Ser Arg His Arg Glu Leu Val Arg Leu Glu Ser Ala Ile Arg Asp Val
237 210 215 220
238 His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
239 225 230 235 240
240 Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
241 245 250 255
242 Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
243 260 265 270
244 Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu Lys
245 275 280 285
247 <210> SEQ ID NO: 7
248 <211> LENGTH: 22
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR primer
255 <400> SEQUENCE: 7
256 ggacgtgttt tccgagaact tg 22
258 <210> SEQ ID NO: 8
259 <211> LENGTH: 22
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: PCR primer
266 <400> SEQUENCE: 8
267 cgaccgtctt ttgtacgttg ag 22
269 <210> SEQ ID NO: 9
270 <211> LENGTH: 16
271 <212> TYPE: PRT
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Peptide linker.
277 <400> SEQUENCE: 9
278 Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Gly Ser
279 1 5 10 15

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/085,188

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Input Set : A:\98-69C1.SEQ.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3